



FIG. 1 - 2

Set II.

V <sub>H</sub> 4-34		D5-5		J <sub>H</sub> 6	
C A R G	V D T A M V	Y Y Y Y		AT TAC TAC TAC	
TGT GCG AGA GG	GTG GAT ACA GCT ATG GTT AC				
C A R G	T P T I R R Y Y			CCL183	
TGT GCG AGA GGA TAC GCG GAT ACA CCT ACC ATT AGA AGA TAC TAT	A D T P V F R R Y Y			CCL240	
C A R G	T P M L K R Y Y			CCL342	
TGT GCG AGA GGC TGG GGG GAT ACA CCT ATG CTT AAA AGA TAC TAC	D D T P M V R R Y Y			AF087422	
C A R A GCA TAC CCG GAT ACA CCT ATG GTC AGG AGG TAC TAC	D D T P M V I K R Y Y			CCL 4B <sup>1</sup>	
C A R G	P P D T V I K R Y Y			AJ239333	
TGT GCG AGA GGC TTC CCG GAT ACA GAT GTG ATT AAG CGC TAC TAC				CCL ID 47 <sup>2</sup>	

3/16

FIG. 1 - 3

Set VIa.

V <sub>H</sub> 1-02				D6-19				J <sub>H</sub> 4						
C	A	R	D/E					Y	F	D	Y			
TGT	GCG	AGA	GA					AC	TAC	TTT	GAC	TAC		
	<u>GG</u>	<u>GTA</u>	<u>TAG</u>	<u>V</u>	<u>Q</u>	<u>W</u>	<u>L</u>							
					<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	<u>C</u>					
C	A	R	E	Q	W	L	V	L	E	H	Y	F	D	Y
TGT	GCG	AGG	GAG	CAG	TGG	CTG	GTA	CTT	GAG	CAC	TAC	TTT	GAC	TAC
C	A	R	V	Q	W	L	G	L	R	-	H	F	D	Y
TGT	GCG	AGA	GTG	CAG	TGG	CTG	GGC	TTA	AGA	---	CAC	TTT	GAC	TAC
C	A	R	E	Q	W	L	G	A	E	-	N	F	D	Y
TGT	GCG	AGA	GAG	CAG	TGG	CTG	GGC	GCA	GAA	---	AAC	TTT	GAC	TAC
C	A	R	E	Q	W	L	V	L	K	-	N	F	D	Y
TGT	GCG	AGG	GAG	CAG	TGG	CTG	GTA	CTG	AAA	---	AAC	TTT	GAC	TAC
C	A	R	V	Q	W	L	L	L	E	-	R	F	D	Y
TGT	GCG	AGA	GTT	CAG	TGG	CTG	TTA	CTC	GAA	---	CGA	TTT	GAC	TAC
C	A	R	N	Q	W	L	G	L	---	D	Y	F	D	Y
TGT	GCG	AGA	AAC	CAG	TGG	CTG	GGT	CTC	---	GAC	TAC	TTT	GAC	TAC
C	A	R	E	Q	W	L	V	R	T	-	S	F	D	Y
TGT	GCG	AGA	GAG	CAG	TGG	CTG	GTA	AGG	ACG	---	AGC	TTT	GAC	TAC

CLL011  
CLL270  
CLL266  
CLL340  
AJ239371  
AJ487492  
U86787

CLL 3<sup>2</sup>  
SMZL Tierens, A.M. U3  
CUL-H2B<sup>1</sup> U0

4/16

## FIG. 1 - 4

Set V1b,c,d

V <sub>H</sub> 1-03				D6-19				J <sub>H</sub> 4			
C	A	R	D/E	C	A	R	D/E	Y	F	D	Y
TGT	GCG	AGA	GA	TGT	GCG	AGA	GA	AC	TAC	TTT	GAC
GG <u>GTA</u> <u>TAG</u> <u>TAG</u> <u>CAG</u> <u>TGG</u> <u>CTG</u> <u>GTA</u> <u>C</u>				GG <u>GTA</u> <u>TAG</u> <u>TAG</u> <u>CAG</u> <u>TGG</u> <u>CTG</u> <u>GTA</u> <u>C</u>				AC TAC TTT GAC TAC			
V				Q				W			
L				L				L			
V				V				V			
CTA				CTA				CTA			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C				C				C			
C</											





7/16

FIG. 1 - 7

Set III.									
V <sub>R</sub> 3-21									
J <sub>R</sub> 6									
C	A	R	E/D						
TGT	GCG	AGA	GA						
Y	Y	Y	Y	Y	G	M	D	V	W
AT	TAC	TAC	TAC	TAC	GGT	ATG	GAC	GTC	TGG
G									
C	A	R	D	A	N	G	M	D	V
TGT	GCG	AGA	GAT	GCG	AAT	GGA	ATG	GAC	GTC
C	A	R	D	R	N	G	M	D	V
TGT	GCG	AGA	GAT	CGG	AAC	GGT	ATG	GAC	GTC
C	A	R	D	Q	N	G	M	D	V
TGT	GCG	AGA	GAT	CAA	AAC	GGT	ATG	GAC	GTC
C	A	S	D	R	N	G	M	D	V
TGT	GCG	AGC	GAT	CGA	AAC	GGT	ATG	GAC	GTC
C	A	R	E	P	Y	G	M	D	V
TGT	GCG	AGA	GAG	CCA	TAC	GGT	ATG	GAC	GTC
C	A	R	D	G	S	G	M	D	V
TGT	GCG	AGA	GAT	GGC	TCC	GGT	ATG	GAC	GTC
C	A	R	D	A	N	G	M	D	V
TGT	GCG	AGA	GAT	GCT	AAC	GGC	ATG	GAC	GTC
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									
G									

8/16

FIG. 1 - 8

Set Vie									
V <sub>E</sub> 5-51 D6-19					J <sub>H</sub> 4				
C	A	R	Q/H		Y	F	D	Y	
TGT	GCG	AGA	CA		AC	TAC	TTT	GAC	TAC
<u>V</u> <u>GTA</u> <u>TAG</u> <u>CAG</u> <u>TGG</u> <u>CTG</u> <u>GTA</u> <u>C</u>									



**FIG. 1 - 9**

9/16

V <sub>H</sub> 1-02				D6-19				J <sub>H</sub> 4								
C	A	R	D/E								F	D	Y			
TGT	GCG	AGA	GA								AC	TTT	GAC	TAC		
		<u>V</u>	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>										
	<u>GG</u>	<u>GTA</u>	<u>TAG</u>	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	<u>C</u>								
C	A	R	E	Q	W	L	V	L	E	H	Y	F	D	Y		
TGT	GCG	AGG	GAG	CAG	TGG	CTG	GTA	CTT	GAG	CAC	TAC	TTT	GAC	TAC	CLL011	
C	A	R	V	Q	W	L	G	L	R	-	H	F	D	Y		
TGT	GCG	AGA	GTC	CAG	TGG	CTG	GGC	TTA	AGA	---	CAC	TTT	GAC	TAC	CLL270	
C	A	R	E	Q	W	L	G	A	E	-	N	F	D	Y		
TGT	GCG	AGA	GAG	CAG	TGG	CTG	GGC	GCA	GAA	---	AAC	TTT	GAC	TAC	CLL266	
C	A	R	E	Q	W	L	V	L	K	-	N	F	D	Y		
TGT	GCG	AGG	GAG	CAG	TGG	CTG	GTA	CTG	AAA	---	AAC	TTT	GAC	TAC	CLL340	
C	A	R	V	Q	W	L	L	L	E	-	R	F	D	Y		
TGT	GCG	AGA	GTT	CAG	TGG	TTA	TTA	CTC	GAA	---	CGA	TTT	GAC	TAC	AJ239371	
C	A	R	N	Q	W	L	G	L	D	-	Y	F	D	Y	CLL 3 <sup>2</sup>	
TGT	GCG	AGA	AAC	CAG	TGG	CTG	GGT	CTC	GAC	---	TAC	TTT	GAC	TAC	AJ487492	
C	A	R	E	Q	W	L	V	R	T	-	S	F	D	Y	SMZL Tierens, A.M.	
TGT	GCG	AGA	GAG	CAG	TGG	CTG	GTA	AGG	ACG	---	AGC	TTT	GAC	TAC	U86787	
C	A	R	E	Q	W	L	V	L	S	-	Y	F	D	Y	CLL-H2B <sup>1</sup> U0	
TGT	GCG	AGG	GAG	CAG	TGG	CTG	GTC	CTA	TCT	---	TAC	TTT	GAC	TAC	CLL336	
C	A	R	E	Q	W	L	V	L	-	N	Y	F	D	Y		
TGT	GCG	AGG	GAG	CAG	TGG	CTG	GTA	CTT	---	AAC	TAC	TTT	GAC	TAC	CLL360	
C	A	R	E	Q	W	L	A	L	K	-	P	F	D	Y		
TGT	GCG	AGA	GAG	CAG	TGG	CTG	GCC	TTA	AAA	---	CCC	TTT	GAC	TAC	AF376961	
C	A	R	K	Q	W	L	A	I	V	N	Y	F	D	Y	LAN Digheiro	
TGT	GCG	AGA	AAG	CAG	TGG	CTG	GCC	ATC	GTC	AAC	TAC	TTT	GAC	TAC	L01278	
C	A	R	E	Q	W	L	G	L	P	-	T	F	D	Y	CLL-412 <sup>3</sup>	
TGT	GCG	AGA	GAG	CAG	TGG	CTG	GGT	CTA	CCT	---	ACC	TTT	GAC	TAC	U86801 <sup>4</sup> U3/1	
C	A	R	V	Q	W	L	G	L	T	G	P	N	D	Y		
TGT	GCT	AGG	GTT	CAG	TGG	CTG	GGC	CTG	ACG	GGG	CCG	AAT	GAC	TAC	U84176	
C	A	R	G	Q	W	L	V	I	L	-	N	F	D	Y	KEM (VH1-46) <sup>5</sup> U0	
TGT	GCG	AGG	GGA	CAG	TGG	CTG	GTC	ATC	CTA	---	AAC	TTT	GAC	TAC	U84162	
C	A	R	D	Q	W	L	P	T	-	N	N	F	D	Y	BYR (VH1-46) <sup>5</sup> U0	
TGT	GCG	AGA	GAT	CAG	TGG	CTG	CCC	ACG	---	AAC	AAC	TTT	GAC	TAC	AF376953	
C	A	R	E	Q	W	L	V	L	S	-	H	F	D	Y	Digheiro PIQ U2	
TGT	GCG	AGG	GAG	CAG	TGG	TTG	GTA	CTA	TCT	---	CAC	TTT	GAC	TAC	CLL154	
C	A	R	Q	Q	W	L	G	G		D	Y	F	D	Y	(VH1-18)	
TGT	GCG	AGG	CAG	CAG	TGG	CTG	GGT	GGC		GAC	TAC	TTT	GAC	TAC	CLL026	
C	A	R	R	Q	W	L	A	L		G	H	F	D	Y		
TGT	GCG	AGA	AGG	CAG	TGG	CTG	GCC	CTA		GGC	CAC	TTT	GAC	TAC	AF099198	
JK2															Tre <sup>11</sup> 012/0-2	
C	A	R	Q	Q	W	F	G	V		Y	Y	F	D	Y		
TGT	GCG	AGA	CAG	CAA	TGG	TTT	GGC	GTG		TAC	TAC	TTT	GAC	TAC	AJ414007	
C	A	R	Q	Q	W	L	V	L		P	Y	F	D	Y	CLL021	
TGT	GCG	AGA	CAG	CAG	TGG	CTG	GTA	CTT		CCA	TAC	TTT	GAC	TAC	Russia U0	
C	A	R	E	Q	W	L	I	V		T	H	F	D	Y	ID38 <sup>2</sup>	
TGT	GCG	AGA	GAG	CAG	TGG	CTC	ATA	GTA		ACT	CAC	TTT	GAC	TAC	AJ555263	
C	A	R	Q	Q	W	L	V	L		D	Y	F	D	Y	GO14	
TGT	GCG	AGA	CAG	CAG	TGG	CTG	GTG	TTG		GAC	TAC	TTT	GAC	TAC	AJ272398	
C	A	R	E	Q	W	L	V	L		S	N	F	D	Y	AG <sup>12</sup>	
Not available																
PH1562																
HOW <sup>13</sup>																

# 10/16

## FIG. 2

### Amino acid alignments of the H chain variable regions of all sequences in each Set

Set	CDR1	CDR2	CDR3
<b>Set IV</b>			
Germline	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALSWVRQAPGQGLEWNGGIIPIFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDVAVYTCARD	YDYVWGSIYR	DAFDVWGQGTMTVTVSS
CELL068	.....	.....	GGD.....SN.....
CELL258	.....	.....	GGI.....PN.....
MF9	.....	.....	GGP.....PN.....
SKT	.....	.....	GGW.....I.....SN.....
CELL022	.....	.....	GGD.....PN.....I
ATE	.....	.....	GGN.....I.....SN.....V.....
Consensus	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALSWVRQAPGQGLEWNGGIIPIFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDVAVYTCARGGDYDYVWGSIYRDAFDVWGQGTMTVTVSS		
<b>Set VIII</b>			
Germline	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALSWVRQAPGQGLEWNGGIIPIFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDVAVYTCARD	DIYVVPAAI	YFYYGMDVWGQGTMTVTVSS
FS41	.....	.....	GG.....MS.....
UCR4	.....	.....	GA.....HG.....
G013	.....	.....	GG.....NR.....
Consensus	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALSWVRQAPGQGLEWNGGIIPIFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDVAVYTCARGGDIYVVPAAI-YFYYGMDVWGQGTMTVTVSS		
<b>Set V</b>			
Germline	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALSWVRQAPGQGLEWNGGIIPIFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDVAVYTCARD	IVRGVIT	YFYYGMDVWGQGTMTVTVSS
CELL561	.....	.....	AM.Q.....QTY.....YM.....K.....
MF21	.....	.....	.....Y.....X.....K.....
RF22	.....	.....	.....Y.....X.....K.....
GH12	.....	.....	.....G.....X.....K.....
FUE	.....	.....	EG.Q.....GI.....
ID64	.....	.....	S.Q.....NVL.....
SIN	.....	.....	.....HLD.....Y.....X.....
Consensus	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALSWVRQAPGQGLEWNGGIIPIFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDVAVYTCARXIVRGVITYFYYGMDVWGQGTMTVTVSS		
<b>Set XII</b>			
Germline	QVQLQNGAGLLKPSSETLSLTCAVYGSGFSGYTHSWIRQPPGKGLWIGINHSSTINPBLKSRVTISVDTSKNQFSLKLSVTAADTAVYTCARG	VDPMV	YFYYGMDVWGQGTMTVTVSS
CELL183	.....	.....	XG.....PTRR.....R.....
CELL240	.....	.....	.....A.I.....YA.....PVPR.....AK.....
CELL342	.....	.....	.....F.....NG.....P.LKR.....L.....
CELL48	.....	.....	.....A.....F.....HS.....R.....K.....AYP.....P.RR.....SVE.....L.....
ID47	.....	.....	.....VD.....DASS.....N.....L.....PP.....DVTK.....F.....
Consensus	QVQLQNGAGLLKPSSETLSLTCAVYGSGFSGYTHSWIRQPPGKGLWIGINHSSTINPBLKSRVTISVDTSKNQFSLKLSVTAADTAVYTCARGYDTPMXXRYFYYGMDVWGQGTMTVTVSS		
<b>Set -VIA</b>			
Germline	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYIMHWVRQAPGQGLEWNGWIPNPGGNTYAKRFQGRVTITRDTSISTAYMELSLRSDTAVYTCARDQMLV	YFDYWGQGTMTVTVSS	
CELL011	.....	.....	H.....LKH.....
CELL266	.....	.....	S.....GAEN.....
CELL270	.....	.....	V.....GLER.....
CELL340	.....	.....	R.....LKN.....
CELL5	.....	.....	V.....LLER.....
CELL18	.....	.....	N.....GLD.....
CELL-H28	.....	.....	E.....RTS.....
Consensus	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYIMHWVRQAPGQGLEWNGWIPNPGGNTYAKRFQGRVTITRDTSISTAYMELSLRSDTAVYTCARDQMLV-YFDYWGQGTMTVTVSS		
<b>Set -VIB</b>			
Germline	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQGLEWNGWIPNPGGNTYAKRFQGRVTITRDTSISTAYMELSLRSDTAVYTCARDQMLV	YFDYWGQGTMTVTVSS	
CELL336	.....	.....	E.....LS.....
CELL360	.....	.....	E.....L.....
LAN	.....	.....	E.....ALK-P.....
CELL-412	.....	.....	K.....ALVN.....
POR	.....	.....	E.....GLP-T.....
PIQ	.....	.....	E.....PTN-N.....
Consensus	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQGLEWNGWIPNPGGNTYAKRFQGRVTITRDTSISTAYMELSLRSDTAVYTCARDQMLV-YFDYWGQGTMTVTVSS		
<b>Set VIC</b>			
Germline	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYISHWVRQAPGQGLEWNGWIPNPGGNTYAKRFQGRVTITRDTSISTAYMELSLRSDTAVYTCARDQMLV	YFDYWGQGTMTVTVSS	
CELL154	.....	.....	E.....LSH.....
<b>Set VID</b>			
Germline	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIMHWVRQAPGQGLEWNGWIPNPGGNTYAKRFQGRVTITRDTSISTAYMELSLRSDTAVYTCARDQMLV	YFDYWGQGTMTVTVSS	
BYR	.....	.....	ILN.....
KRM	.....	.....	VGLTGN.....
Consensus	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIMHWVRQAPGQGLEWNGWIPNPGGNTYAKRFQGRVTITRDTSISTAYMELSLRSDTAVYTCARGQMKKKKKEDYWGQGTMTVTVSS		
<b>Set VIE</b>			
Germline	QVQLVQSGAEVKKPGSLRISCKSGSYFTSYIMHWVRQMPGKGLWNGRIDPDSYTNYSBPFQGHVITISADKSIISTAYLQWSSLRASDTAVYTCARDQMLV	YFDYWGQGTMTVTVSS	
CELL026	.....	.....	GGD.....
TR8	.....	.....	ALCH.....
CELL021	.....	.....	PGVY.....
ID38	.....	.....	LP.....
G014	.....	.....	TVTH.....
AG	.....	.....	LD.....
HOW	.....	.....	LSN.....
Consensus	QVQLVQSGAEVKKPGSLRISCKSGSYFTSYIMHWVRQMPGKGLWNGRIDPDSYTNYSBPFQGHVITISADKSIISTAYLQWSSLRASDTAVYTCARDQMLV-YFDYWGQGTMTVTVSS		

11/16  
FIG. 3*Amino acid alignments of the L chain variable regions of all sequences in each Set.*

<b>Set IV</b>				
Germ line	CDR1	CDR2	CDR3	
CUJ068	EIVLTQSPGTLISLPGERATLS	CRASQSVSSSYLA	NTQKPGQAPRLIYGAS	SRATGTPDRFSGSGSGTDFTLTISRLPE
CUJ258	.....	.....	.....	FAVYTCQQYGS
MF9	.....	.....	.....	SPFTFGQTKV
Consensus	EIVLTQSPGTLISLPGERATLS	CRASQSVSSSYLA	NTQKPGQAPRLIYGAS	SRATGTPDRFSGSGSGTDFTLTISRLPE
				FAVYTCQQYGS
				SPFTFGQTKV
<b>Set VIII</b>				
Germ line	CDR1	CDR2	CDR3	
GO13	EIVLTQSPATLSLPGERATLS	CRASQSVSSSYLA	NTQKPGQAPRLIYDAS	SRATGTPDRFSGSGSGTDFTLTISRLPE
	.....	.....	.....	FAVYTCQQRSNTFG
				SPFTFGTKVDIK
				.....G
<b>Set V</b>				
Germ line	CDR1	CDR2	CDR3	
RP22	QSVLTQPPSLSGTGGRTIS	CGSSGNTGNTVWYQQL	PGTAPKLLIYNNQ	RFGVDRFSGSGSGTASLAISGLQSE
GN12	.....	.....	.....	DEADYTCANWDDSLNG
Consensus	QSVLTQPPSLSGTGGRTIS	CGSSGNTGNTVWYQQL	PGTAPKLLIYNNQ	RFGVDRFSGSGSGTASLAISGLQSE
				DEADYTCANWDDSLNG
				XTGGTKLV
<b>Set I</b>				
Germ line	CDR1	CDR2	CDR3	
CUJ183	DVMTQSPFLSLPVTLGQ	PASISCRSSQSLVYSDGNTYLN	WQRPQGSPRLIYKVN	RDSDGVDRFSGSGSGTDFTLKISR
CUJ240	.....	.....	.....	VEADVGVYTCMQGTHWPF
CUJ342	.....	.....	.....	YTFGQTKLEIK
Consensus	DVMTQSPFLSLPVTLGQ	PASISCRSSQSLVYSDGNTYLN	WQRPQGSPRLIYKVN	RDSDGVDRFSGSGSGTDFTLKISR
				VEADVGVYTCMQGTHWPF
				YTFGQTKLEIK
				.....V
				.....W
<b>Set VI</b>				
Germ line	CDR1	CDR2	CDR3	
CUJ011	DIQMTQSPSSLSASVGRVTIT	CRASQSISSYLNWYQKPG	KAPKLLIYAASLIQSG	SVDRFSGSGSGTDFTLTISLQPED
CUJ266	.....	.....	.....	FAVYTCQQSYSTFP
CUJ270	.....	.....	.....	WTFGQTKV
CUJ340	.....	.....	.....	.....K
CUJ336	.....	.....	.....	.....I
CUJ360	.....	.....	.....	.....I
CUJ-412	.....	.....	.....	.....I
CUJ154	.....	.....	.....	.....I
TFE	.....	.....	.....	.....I
GO14	.....	.....	.....	.....I
Consensus	DIQMTQSPSSLSASVGRVTIT	CRASQSISSYLNWYQKPG	KAPKLLIYAASLIQSG	SVDRFSGSGSGTDFTLTISLQPED
				FAVYTCQQSYSTFP
				WTFGQTKLEIK

12/16  
FIG. 4

V <sub>β</sub> 1-69		D3-16		J <sub>H</sub> 3		V <sub>K</sub> A27		J <sub>K</sub> 1/4*/5 <sup>#</sup>	
C A R D/E		D A F D I		Q Q Y G S S P P		Q Q Y G S S P P		Q Q Y G S S P P	
tgt ggc aga ga		t gat gct ttt gat atc		cag cag tat ggt ago tca cct cc		cag cag tat ggt ago tca cct cc		cag cag tat ggt ago tca cct cc	
Y Y D Y V W G S Y R Y		S N		C L L 0 6 8		C L L 0 6 8		C L L 0 6 8	
g tat tat gat tac gtt tgg ggg agt tat cgt tat acc		P N		C L L 2 5 8		C L L 2 5 8		C L L 2 5 8	
G G D		P N		M F 9		M F 9		M F 9	
G G I		S N		S M I		S M I		S M I	
G G P		P N		C L L 0 2 2 (natural Ab producing clone)		C L L 0 2 2 (natural Ab producing clone)		C L L 0 2 2 (natural Ab producing clone)	
G G N		S N		α-cardiolipin		α-cardiolipin		α-cardiolipin	
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							
G G P		P N							
G G N		S N							
G G D		P N							
G G I		S N							

13/16  
FIG. 5

[illegible]



V <sub>H</sub> 4-34	D5-5	JH6	V <sub>K</sub> A17	J <sub>K</sub> 1/2*
C A R G		Y Y Y	M Q G T H W P P	
tgt ggg aga gg		at tac tac tac	atg caa ggt aca cac tgg cct cc	
V D T A M V			W T F G	
gtg gat aca gct atg gtt ac			g tgg agg ttc ggc	
Y G . . P T I R . . C L L 183		. . . . . ga aga . . . . t	. . . . .	. . . . .
. . . . . a tac .g. . . . . c.. cc a..		. . . . .	. . . . .	. . . . .
. . . . . Y A . . P V F R R . . C L L 240		. . . . .	. . . . .	. . . . .
. . . . . a tat .c. . . . . b c., g.. t.. cgg cg.		. . . . .	. . . . .	. . . . .
. . . . . W G . . P . L K R . . C L L 342		. . . . .	. . . . .	. . . . .
. . . . . .c tgg .g. . . . . c.. .. a aga . . . .		. . . . .	. . . . .	. . . . .
. . . . . A Y P . . P . V R R . . C L L 4B		. . . . .	. . . . .	. . . . .
. . . . . .ca tac cc. . . . . c.. .. .c .gg agg . . . .		. . . . .	. . . . .	. . . . .
. . . . . F P . . D V I K R . . ID47		. . . . .	. . . . .	. . . . .
. . . . . .c ttc cc. . . . . a.g.. a.. .g cg. . . .		. . . . .	. . . . .	. . . . .
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15			1 2 3 4 5 6 7 8 9 10 11 12	

16/16  
FIG. 8

V <sub>H</sub> 1-02	D6-19	J <sub>H</sub> 4	V <sub>K</sub> 012/02	J <sub>K</sub> 1/2*
CARD/E		YFDY	QQSYSTPP	WTFG
tgt gcg aga ga		ac tac ttt gac tac	caa cag agt tac agt acc cct cc	g tgg acg tto ggc
V * QWLV				
gg gta tag cag tgg atg gta c				
...	LEH	...	CLL011	...
...	GAE-N	...	CLL266	...
...	GLR-H	...	CLL270	...
...	LK-N	...	CLL340	...
...	LLE-R	...	CLL3	...
...	GLD	...	slv18 (marginal zone lymphoma)	...
...	RT-S	...	CLL-H2B	...
...	LS-	...	CLL336	...
...	L-N	...	CLL360	...
...	ALK-P	...	LAN	...
...	AIVN	...	CLL-412	...
...	PT-NN	...	PIQ	...
...	LS-H	...	CLL154	...
...	IL-N	...	BYR	...
...	GLTGPN	...	KEM	...
...	GG-D	...	CLL026	...
...	AL-GH	...	TRE	...
...	FGV-Y	...	CLL021	...
...	LP-	...	ID38	...
...	IVT-H	...	GO14	...
...	L-D	...	AG	...
...	LS-	...	HOW	...
nucleotide sequence not available				
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15			1 2 3 4 5 6 7 8 9 10 11 12 13	